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 NEWS  5  AUG 24  CA/CAplus enhanced with legal status information for
                  U.S. patents
 NEWS  6  SEP 09  50 Millionth Unique Chemical Substance Recorded in
                  CAS REGISTRY
 NEWS  7  SEP 11  WPIDS, WPINDEX, and WPIX now include Japanese FTERM
                  thesaurus

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=> s yeast (3a) (mate or mating)
L1        2254 YEAST (3A) (MATE OR MATING)

=> s l1 and meiosis
L2          65 L1 AND MEIOSIS

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3           44 DUP REM L2 (21 DUPLICATES REMOVED)

=> s l3 and py<=2001
L4          33 L3 AND PY<=2001

=> s l3 and py<=2002
L5          34 L3 AND PY<=2002

=> d bib abs 1-
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L5   ANSWER 1 OF 34  BIOSIS  COPYRIGHT (c) 2009 The Thomson
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AN   2001:72729  BIOSIS
DN   PREV200100072729
TI   Serotype AD strains of Cryptococcus neoformans are diploid or
aneuploid
     and are heterozygous at the mating-type locus.
AU   Lengeler, Klaus B.; Cox, Gary M.; Heitman, Joseph [Reprint
author]
CS   Department of Genetics, Duke University Medical Center, Research
Dr., 322
     CARL Bldg., Durham, NC, 27710, USA
     heitm001@duke.edu
SO   Infection and Immunity, (January, 2001) Vol. 69, No. 1, pp.
     115-122. print.
     CODEN: INFIBR. ISSN: 0019-9567.
DT   Article
LA   English
```

ED Entered STN: 7 Feb 2001
Last Updated on STN: 12 Feb 2002
AB Cryptococcus neoformans is a pathogenic basidiomycete with a defined
sexual cycle involving mating between haploid yeast
cells with a transient diploid state. C. neoformans occurs in four
predominant serotypes (A, B, C, and D), which represent different
varieties or species. Rare clinical and environmental isolates with an
unusual AD serotype have been reported and suggested to be diploid. We
found by fluorescence-activated cell sorter analysis that serotype AD
strains are aneuploid or diploid. PCR analysis with primers specific for
serotype A or D alleles of the CNA1, CLA4, and GPA1 genes revealed that
both alleles are often present in serotype AD strains. PCR analysis with
primers specific for genes in the MATa or MATalpha mating-type loci
revealed that serotype AD strains are heterozygous for the mating-type
locus. Interestingly, in several serotype AD strains, the MATalpha locus
was derived from the serotype D parent and the MATa locus was inherited
from a serotype A parent that has been thought to be extinct.
Basidiospores from a self-fertile serotype AD strain bearing the putative
serotype A MATa locus showed a very low viability (apprx5%), and no
fertile serotype A MATa strain could be recovered. Serotype AD strains
were virulent in a murine model. Hybrid AD strains could readily be
isolated following a laboratory cross between a serotype A strain and a
serotype D strain. In summary, serotype AD strains of C. neoformans are
unusual aneuploid or diploid strains that result from matings between
serotype A and D strains. Self-fertile isolates fail to undergo normal
meiosis because of genetic divergence. Our findings further
suggest that serotype A MATa strains may exist in nature.

L5 ANSWER 2 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2000:387716 BIOSIS
DN PREV200000387716

TI Schizosaccharomyces pombe Ste7p is required for both promotion and withholding of the entry to meiosis.
AU Matsuyama, Akihisa; Yabana, Naoyuki; Watanabe, Yoshinori; Yamamoto, Masayuki [Reprint author]
CS Department of Biophysics and Biochemistry, Graduate School of Science, University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo, 113-0033, Japan
SO Genetics, (June, 2000) Vol. 155, No. 2, pp. 539-549. print. CODEN: GENTAE. ISSN: 0016-6731.
DT Article
LA English
OS Genbank-AB036789; DDBJ-AB036789
ED Entered STN: 13 Sep 2000
Last Updated on STN: 8 Jan 2002
AB The fission yeast ste7 mutant cannot mate and undergo meiosis, but shows no defect in vegetative growth. We cloned and characterized the ste7 gene. The deduced ste7 gene product (Ste7p) was a protein of 569 amino acids with no significant similarity to other proteins. Transcription of ste7 was induced by nutrient starvation via the function of the transcription factor Ste11p. Disruption of the ste7 gene blocked both conjugation and meiosis, showing that Ste7p plays a positive role in these two processes, probably activating the pheromone signal pathway. Unexpectedly, overexpression of ste7+ promoted conjugation but inhibited meiosis in wild-type cells. The temperature-sensitive pat1-114 mutant underwent ectopic conjugation at the semirestrictive temperature when its genetic background was ste7+, whereas the same mutant initiated haploid meiosis when its genetic background was ste7DELTA. Two-hybridanalysis suggested that Ste7p interacts physically with both Pat1p and Mei2p, which together constitute the major switch to initiate meiosis. Ste7p tagged with green fluorescent protein accumulated in haploid cells under nutrient starvation until they completed conjugation, but this protein disappeared when they were to enter meiosis. These observations suggest that Ste7p may have a function to suppress the onset of meiosis until the conjugation process has been duly completed.

L5 ANSWER 3 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 1999:444529 BIOSIS
DN PREV199900444529
TI Multiple sex pheromones and receptors of a mushroom-producing fungus
elicit mating in yeast.
AU Fowler, Thomas J.; DeSimone, Susan M.; Mitton, Michael F.; Kurjan, Janet;
Raper, Carlene A. [Reprint author]
CS Department of Microbiology and Molecular Genetics, University of Vermont,
Burlington, VT, 05405, USA
SO Molecular Biology of the Cell, (Aug., 1999) Vol. 10, No. 8, pp. 2559-2572. print.
CODEN: MBCEEV. ISSN: 1059-1524.
DT Article
LA English
ED Entered STN: 26 Oct 1999
Last Updated on STN: 26 Oct 1999
AB The mushroom-producing fungus Schizophyllum commune has thousands of
mating types defined, in part, by numerous lipopeptide pheromones and
their G protein-linked receptors. Compatible combinations of pheromones
and receptors encoded by different mating types regulate a pathway of
sexual development leading to mushroom formation and meiosis. A
complex set of pheromone-receptor interactions maximizes the likelihood of
outbreeding; for example, a single pheromone can activate more than one
receptor and a single receptor can be activated by more than one
pheromone. The current study demonstrates that the sex pheromones and
receptors of Schizophyllum, when expressed in Saccharomyces cerevisiae,
can substitute for endogenous pheromone and receptor and induce the yeast
pheromone response pathway through the yeast G protein. Secretion of
active Schizophyllum pheromone requires some, but not all, of the
biosynthetic machinery used by the yeast lipopeptide pheromone a-factor.
The specificity of interaction among pheromone-receptor pairs in
Schizophyllum was reproduced in yeast, thus providing a powerful system
for exploring molecular aspects of pheromone-receptor interactions for a
class of seven-transmembrane-domain receptors common to a wide range of
organisms.

L5 ANSWER 4 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1999:37311 BIOSIS
DN PREV199900037311
TI The mating-type proteins of fission yeast induce meiosis by directly activating mei3 transcription.
AU van Heeckeren, Willem J.; Dorris, David R.; Struhl, Kevin [Reprint author]
CS Dep. Biological Chemistry Molecular Pharmacology, Harvard Med. Sch., 240 Longwood Avenue, Boston, MA 02115-5730, USA
SO Molecular and Cellular Biology, (Dec., 1998) Vol. 18, No. 12, pp. 7317-7326. print.
CODEN: MCEBD4. ISSN: 0270-7306.
DT Article
LA English
ED Entered STN: 3 Feb 1999
Last Updated on STN: 3 Feb 1999
AB Cell type control of meiotic gene regulation in the budding yeast Saccharomyces cerevisiae is mediated by a cascade of transcriptional repressors, a1-alpha2 and Rme1. Here, we investigate the analogous regulatory pathway in the fission yeast Schizosaccharomyces pombe by analyzing the promoter of mei3, the single gene whose expression is sufficient to trigger meiosis. The mei3 promoter does not appear to contain a negative regulatory element that represses transcription in haploid cells. Instead, correct regulation of mei3 transcription depends on a complex promoter that contains at least five positive elements upstream of the TATA sequence. These elements synergistically activate mei3 transcription, thereby constituting an on-off switch for the meiosis pathway. Element C is a large region containing multiple sequences that resemble binding sites for Mc, an HMG domain protein encoded by the mating-type locus. The function of element C is extremely sensitive to spacing changes but not to linker-scanning mutations, suggesting the possibility that Mc functions as an architectural transcription factor. Altered-specificity experiments indicate that element D interacts with Pm, a homeodomain protein encoded by the mating-type locus. This indicates that Pm functions as a direct activator of the meiosis pathway, whereas the homologous mating-type protein in S. cerevisiae (alpha2) functions as a repressor.

Thus, despite the strong similarities between the mating-type loci of S.
cerevisiae and S. pombe, the regulatory logic that governs the tight
control of the key meiosis-inducing genes in these organisms is completely different.

L5 ANSWER 5 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1998:439319 BIOSIS
DN PREV199800439319
TI Homothallic life cycle in the diploid red yeast Xanthophyllomyces,
dendrorhous (Phaffia rhodozyma).
AU Kucsera, J. [Reprint author]; Pfeiffer, I.; Fernczy, L.
CS Dep. Microbiol., Jozsef Attila Univ., Szeged, Hungary H-6701, Szeged, P.O.
Box 533, Hungary
SO Antonie van Leeuwenhoek, (Feb., 1998) Vol. 73, No. 2, pp. 163-168. print.
CODEN: ALJMAO. ISSN: 0003-6072.
DT Article
LA English
ED Entered STN: 7 Oct 1998
Last Updated on STN: 7 Oct 1998
AB Sexual activity was induced in the basidiomyceteous Phaffia rhodozyma
(Xanthophyllomyces dendrorhous) by depletion of nitrogen from the culture
medium. This activity involved both mating between two
yeast cells and the formation of basidiospores. Mating is
possibly started by a G1 phase arrest of the cell cycle, as in other
yeasts. The life cycle exhibited homothallic features. Crosses between
genetically marked strains, and pulse-field gel electrophoresis of the
chromosomal DNA of cells derived from individual spores revealed evidence
of karyogamy, meiosis and even recombination. The segregation
ratio in tetrads pointed to diploid vegetative cells, which formed
tetraploid zygotes and the immediate meiosis then gave rise to
diploid progenies again. Apart from the type strain Phaffia rhodozyma CBS
5905, all the examined strains were able to sporulate.

L5 ANSWER 6 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1998:303215 BIOSIS
DN PREV199800303215
TI The tup1-Ssn6 general repressor is involved in repression of IME1 encoding

a transcriptional activator of meiosis in Saccharomyces cerevisiae.
AU Mizuno, Takayuki [Reprint author]; Nakazawa, Nobushige; Remsgsamrarn, Panan; Kunoh, Tatsuki; Oshima, Yasuji; Harashima, Satoshi
CS Dep. Biotechnol., Graduate Sch. Eng., Osaka Univ. Yamadaoka 2-1, Suta-shi, Osaka 565-0871, Japan
SO Current Genetics, (April, 1998) Vol. 33, No. 4, pp. 239-247. print.
CODEN: CUGED5. ISSN: 0172-8083.
DT Article
LA English
ED Entered STN: 15 Jul 1998
Last Updated on STN: 15 Jul 1998
AB Ime1 plays a pivotal role in the initiation of meiosis in a/alpha diploid cells of Saccharomyces cerevisiae. In the absence of glucose and nitrogen, IME1 expression is greater in a/alpha cells than in either a or a cells and therefore only a/a, but not alpha/alpha or alpha/alpha, cells are committed to sporulation. It is known that IME1 expression is positively regulated by Mck1, Rim1, Ime4 and the Swi-Snf complex but other factors may also be involved. In addition, Rme1 is assumed to repress IME1 expression. To provide more details of the repression of expression of IME1, we have isolated mutants in which the IME1p-PH05 fusion gene integrated at the ura3 locus is expressed in a cells under nutritionally rich conditions. We found that mutations occurred in TUP1, SSN6, SIN4 and RGR1, among which TUP1 and SSN6 were identified for the first time as negative regulators of IME1 expression. Deletion of the Rme1-binding site from the IME1 promoter did not result in activation of the expression of IME1 under nutritionally rich conditions, suggesting that Rme1 does not function as a DNA-binding protein with the Tup1-Ssn6 repression complex. We also demonstrated that the 294-bp fragment from nucleotide position -914 to -621 and the 301-bp fragment from nucleotide position -1215 to -915 of the IME1 promoter region contain

elements acting as URS and UAS in TUP1+ and tup1 mutant cells, respectively. These findings indicate that IME1 is negatively regulated by the Tup1-Ssn6 repressor complex through two distinct upstream regions in conjunction with unidentified-DNA-binding proteins.

L5 ANSWER 7 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1997:332262 BIOSIS
DN PREV199799631465
TI Isolation of yeast mutants hypersensitive to mating pheromones.
AU Davis, Kevin; Davey, John
CS Dep. Biol. Sci., Univ. Warwick, Coventry CV4 7AL, UK
SO Biochemical Society Transactions, (1997) Vol. 25, No. 2, pp. 227S.
Meeting Info.: 660th Meeting of the Biochemical Society, Joint Congress with the British Society for Immunology. Harrogate, England, UK. December 10-13, 1996.
CODEN: BCSTB5. ISSN: 0300-5127.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 5 Aug 1997
Last Updated on STN: 5 Aug 1997

L5 ANSWER 8 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1996:380717 BIOSIS
DN PREV199699103073
TI Chromosomal inheritance of epigenetic states in fission yeast during mitosis and meiosis.
AU Grewal, Shiv I. S.; Klar, Amar J. S.
CS Gene Regulation, Chromosome Biol. Lab., ABL-Basic Res. Program, Natl. Cancer Inst.-Frederick Cancer Res. Dev. Cent., Frederick, MD 21702-1201, USA
SO Cell, (1996) Vol. 86, No. 1, pp. 95-101.
CODEN: CELLB5. ISSN: 0092-8674.
DT Article
LA English
ED Entered STN: 26 Aug 1996
Last Updated on STN: 26 Aug 1996
AB Inheritance of the active and inactive states of gene expression by individual cells is crucial for development. In fission yeast, mating-type region consists of three loci called mat1, mat2, and

mat3. Transcriptionally silent mat2 and mat3 loci are separated by a 15 kb interval, designated the K-region, and serve as donors of information for transcriptionally active mat1 interconversion. In a strain carrying replacement of 7.5 kb of the K-region with the ura4 gene, we discovered that ura4 silencing and efficiency of mating-type switching were covariegated and were regulated by an epigenetic mechanism. Genetic analyses demonstrated that epigenetic states were remarkably stable not only in mitosis but also in meiosis and were linked to the mating-type region. This study indicates that different epigenetic states are heritable forms of chromatin organization at the mat region.

L5 ANSWER 9 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1994:256854 BIOSIS
DN PREV199497269854
TI Mutations in XRS2 and RAD50 delay but do not prevent mating-type switching in Saccharomyces cerevisiae.
AU Ivanov, Evgeny L.; Sugawara, Neal; White, Charles I.; Fabre, Francis; Haber, James E. [Reprint author]
CS Rosenstiel Cent., Brandeis Univ., Waltham, MA 02254-9110, USA
SO Molecular and Cellular Biology, (1994) Vol. 14, No. 5, pp. 3414-3425.
CODEN: MCEBD4. ISSN: 0270-7306.
DT Article
LA English
ED Entered STN: 8 Jun 1994
Last Updated on STN: 8 Jun 1994
AB In Saccharomyces cerevisiae, a large number of genes in the RAD52 epistasis group has been implicated in the repair of chromosomal double-strand breaks and in both mitotic and meiotic homologous recombination. While most of these genes are essential for yeast mating-type (MAT) gene switching, neither RAD50 nor XRS2 is required to complete this specialized mitotic gene conversion process.
Using a galactose-inducible HO endonuclease gene to initiate MAT switching, we have examined the effect of null mutations of RAD50 and of XRS2 on intermediate steps of this recombination event. Both rad50 and xrs2 mutants exhibit a marked delay in the completion of switching. Both mutations reduce the extent of 5'-to-3' degradation from the end of the

HO-created double-strand break. The steps of initial strand invasion and
new DNA synthesis are delayed by approximately 30 min in mutant cells.
However, later events are still further delayed, suggesting that XRS2 and
RAD50 affect more than one step in the process. In the rad50 xrs2 double
mutant, the completion of MAT switching is delayed more than in either
single mutant, without reducing the overall efficiency of the process.
The XPS2 gene encodes an 854-amino-acid protein with no obvious similarity
to the Rad50 protein or to any other protein in the database.
Overexpression of RAD50 does not complement the defects in xrs2 or vice
versa.

L5 ANSWER 10 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN
AN 1992:475930 BIOSIS
DN PREV199294107305; BA94:107305
TI GENE CONVERSION IN THE ESCHERICHIA-COLI RECF PATHWAY A SUCCESSIVE HALF
CROSSING-OVER MODEL.
AU YAMAMOTO K [Reprint author]; KAUSANO K; TAKAHASHI N K; YOSHIKURA H;
KOBAYASHI I
CS DEP MOL BIOL, INST MED SCI, UNIV TOKYO 4-6-1 SHIROGANEDAI, TOKYO 108, JPN
SO Molecular and General Genetics, (1992) Vol. 234, No. 1, pp. 1-13.
CODEN: MGGEAE. ISSN: 0026-8925.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 27 Oct 1992
Last Updated on STN: 27 Oct 1992
AB Gene conversion - apparently non-reciprocal transfer of sequence
information between homologous DNA sequences - has been reported in
various organisms. Frequent association of gene conversion with
reciprocal exchange (crossing-over) of the flanking sequences in
meiosis has formed the basis of the current view that gene
conversion reflects events at the site of interaction during homologous
recombination. In order to analyze mechanisms of gene conversion and
homologous recombination in an Escherichia coli strain with an active RecF

pathway (recBC sbcBC), we first established in cells of this strain a plasmid carrying two mutant neo genes, each deleted for a different gene segment, in inverted orientation. We then selected kanamycin-resistant plasmids that had reconstituted an intact neo+ gene by homologous recombination. We found that all the neo+ plasmids from these clones belonged to the gene-conversion type in the sense that they carried one neo+ gene and retained one of the mutant neo genes. This apparent gene conversion was, however, only very rarely accompanied by apparent crossing-over of the flanking sequences. This is in contrast to the case in a rec+ strain or in a strain with an active RecE pathway (recBC sbcA).

Our further analyses, especially comparisons with apparent gene conversion in the rec+ strain, led us to propose a mechanism for this biased gene conversion. This "successive half crossing-over model" proposes that the elementary recombinational process is half crossing-over in the sense that it generates only one recombinant DNA duplex molecule, and leaves one or two free end(s), out of two parental DNA duplexes. The resulting free end is, the model assumes, recombinogenic and frequently engages in a second round of half crossing-over with the recombinant duplex. The products resulting from such interaction involving two molecules of the plasmid would be classified as belonging to the gene-conversion type without crossing-over. We constructed a dimeric molecule that mimics the intermediate form hypothesized in this model and introduced it into cells.

Biased gene conversion products were obtained in this reconstruction experiment. The half crossing-over mechanism can also explain formation of huge linear multimers of bacterial plasmids, the nature of transcribable recombination products in bacterial conjugation, chromosomal gene conversion not accompanied by flanking exchange (like that in mating-type switching), and antigenic variation in microorganisms.

L5 ANSWER 11 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1988:229643 BIOSIS
DN PREV198834112163; BR34:112163
TI A SPECIFIC INHIBITOR OF THE RAN1-POSITIVE PROTEIN KINASE REGULATES ENTRY INTO MEIOSIS IN SCHIZOSACCHAROMYCES-POMBE.
AU MCLEOD M [Reprint author]; BEACH D
CS COLD SPRING HARBOR LAB, PO BOX 100, COLD SPRING HARBOR, NY 11724, USA
SO Nature (London), (1988) Vol. 332, No. 6164, pp. 509-514.
CODEN: NATUAS. ISSN: 0028-0836.
DT Article
FS BR
LA ENGLISH
ED Entered STN: 9 May 1988
Last Updated on STN: 9 May 1988

L5 ANSWER 12 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1988:221853 BIOSIS
DN PREV198885111088; BA85:111088
TI THE SPORULATION CAPABLE SCA MUTATION OF SACCHAROMYCES-CEREVISIAE IS AN ALLELE OF THE SIR-2 GENE.
AU MARGOLSKEE J P [Reprint author]
CS DEP BIOCHEM BIOPHYSICS, UNIV CALIF, SAN FRANCISCO, CALIF, USA
SO Molecular and General Genetics, (1988) Vol. 211, No. 3, pp. 430-434.
CODEN: MGGEAE. ISSN: 0026-8925.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 4 May 1988
Last Updated on STN: 4 May 1988
AB We have used the special properties of the spo13-1 mutation in order to study the regulation of yeast meiosis by the mating type loci. We have found that both the rme1-1 mutation and the sca mutation allow haploid meiosis in spo13-1 strains. Therefore, haploid meiosis is regulated in the same manner as diploid meiosis. Unlike rme1-1, the sca mutations allows meiosis through derepression of the silent mating type cassettes; sca strains can sporulate only because they express both MATa and MATα information. We have found further that sca is an allele of SIR2, one of the genes involved in repression of the silent cassettes.

Therefore, the RME1 gene is the only known candidate for a master negative
regulator through which the MAT locus controls meiosis.

L5 ANSWER 13 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN
AN 1987:484326 BIOSIS
DN PREV198784118969; BA84:118969
TI INSERTIONS OF UP TO 17 AMINO ACIDS INTO A REGION OF ALPHA TUBULIN DO NOT
DISRUPT FUNCTION IN-VIVO.
AU SCHATZ P J [Reprint author]; GEORGES G E; SOLOMON F; BOTSTEIN D
CS DEP BIOL, MASS INST TECHNOL, CAMBRIDGE, MASS 02139, USA
SO Molecular and Cellular Biology, (1987) Vol. 7, No. 10, pp.
3799-3805.
CODEN: MCEBD4. ISSN: 0270-7306.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 17 Nov 1987
Last Updated on STN: 17 Nov 1987
AB Microtubules in yeasts are essential components of the mitotic and meiotic
spindles and are necessary for nuclear movement during cell division and
mating. The yeast Saccharomyces cerevisiae has two α-tubulin genes,
TUB1 and TUB3, either of which alone is sufficient for these processes
when present in a high enough copy number. Comparisons of sequences from
several species reveals the presence of a variable region near the amino
terminus of α-tubulin proteins. We perturbed the structure of this
region in TUB3 by inserting into it 3, 9, or 17 amino acids and tested the
ability of these altered proteins to function as the only α-tubulin
protein in yeast cells. We found that each of these altered proteins was
sufficient on its own for mitotic growth, mating, and
meiosis of yeast. We conclude that this region can
tolerate considerable variation without losing any of the highly conserved
functions of α-tubulin. Our results suggest that variability in
this region occurs because it can be tolerated, not because it specifies
an important function for the protein.

L5 ANSWER 14 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on

STN
AN 1987:390118 BIOSIS
DN PREV198733070258; BR33:70258
TI INDIRECT CONTROL OF SPORULATION BY THE MATING TYPE LOCUS IN YEAST.
AU MITCHELL A P [Reprint author]
CS DEP BIOCHEMISTRY AND BIOPHYSICS, UNIV CALIFORNIA AT SAN FRANCISCO, SAN
FRANCISCO, CALIF 94143, USA
SO UCLA Symp. Mol. Cell. Biol., New Ser., (1987) pp. 147-158.
GRANNER, D., M. G. ROSENFELD AND S. CHANG (ED.). UCLA (UNIVERSITY OF
CALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY NEW
SERIES, VOL. 52. TRANSCRIPTIONAL CONTROL MECHANISMS; CETUS-UCLA
CONFERENCE, KEYSTONE, COLORADO, USA, APRIL 6-13, 1986. XX+496P.
ALAN R.
LISS, INC.: NEW YORK, NEW YORK, USA. ILLUS.
Publisher: Series: UCLA (University of California Los Angeles) Symposia on
Molecular and Cellular Biology New Series.
CODEN: USMBD6. ISSN: 0735-9543. ISBN: 0-8451-2651-2.
DT Book
Conference; (Meeting)
FS BR
LA ENGLISH
ED Entered STN: 12 Sep 1987
Last Updated on STN: 12 Sep 1987

L5 ANSWER 15 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN
AN 1986:408078 BIOSIS
DN PREV198631084044; BR31:84044
TI REGULATION OF MEIOSIS IN YEAST BY THE MATING TYPE LOCUS AND THE PRODUCT OF THE RME-1 GENE.
AU MITCHELL A [Reprint author]; HERSKOWITZ I
CS DEP BIOCHEM BIOPHYSICS, UNIV CALIF, SAN FRANCISCO, CA 94143, USA
SO Journal of Cellular Biochemistry Supplement, (1986) No. 10 PART D, pp. 87.
Meeting Info.: SYMPOSIUM ON TRANSCRIPTIONAL CONTROL MECHANISMS HELD AT THE
15TH ANNUAL MEETING OF THE UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES)
SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, APR. 6-13, 1986. J CELL
BIOCHEM SUPPL.
ISSN: 0733-1959.
DT Conference; (Meeting)
FS BR
LA ENGLISH
ED Entered STN: 14 Oct 1986

Last Updated on STN: 14 Oct 1986

L5 ANSWER 16 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1982:107396 BIOSIS
DN PREV198223037388; BR23:37388
TI THE CONTROL OF CELL TYPE BY THE MATING TYPE LOCUS IN YEAST.
AU NASMYTH K [Reprint author]; TATCHELL K
CS COLD SPRING HARBOR LAB, COLD SPRING HARBOR, NY 11724, USA
SO Journal of Supramolecular Structure and Cellular Biochemistry, (1981) No. SUPPL. 5, pp. 403.
Meeting Info.: MEETING ON DEVELOPMENTAL BIOLOGY USING PURIFIED GENES
PRESENTED AT THE ICN-UNIVERSITY OF CALIFORNIA AT LOS ANGELES SYMPOSIA ON
MOLECULAR AND CELLULAR BIOLOGY, MARCH 15-20, 1981. J SUPRAMOL STRUCT CELL
BIOCHEM.
CODEN: JSSBDH. ISSN: 0275-3723.
DT Conference; (Meeting)
FS BR
LA ENGLISH

L5 ANSWER 17 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1981:288463 BIOSIS
DN PREV198172073447; BA72:73447
TI GENE CONVERSION BETWEEN DUPLICATED GENETIC ELEMENTS IN YEAST SACCHAROMYCES-CEREVISIAE.
AU JACKSON J A [Reprint author]; FINK G R
CS SECTION BIOCHEMISTRY, MOLECULAR, CELL BIOL, WING HALL, CORNELL UNIV,
ITHACA, NEW YORK 14853, USA
SO Nature (London), (1981) Vol. 292, No. 5821, pp. 306-311.
CODEN: NATUAS. ISSN: 0028-0836.
DT Article
FS BA
LA ENGLISH
AB The mitotic recombination behavior of a duplication of the his4 region on
chromosome III in the yeast S. cerevisiae was studied. The major recombination event between the duplicated segments is gene conversion
unassociated with reciprocal recombination. The rad52-1 mutation preferentially decreases mitotic gene conversion. Mitotic gene conversion
may occur by a different pathway from that occurring in meiosis. This mitotic gene conversion may be important in yeast mating type interconversion and maintenance of sequence

homogeneity in families of repeated eukaryotic genes.

L5 ANSWER 18 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1978:214724 BIOSIS
DN PREV197866027221; BA66:27221
TI ZYGOTE FORMATION AND RECOMBINATION BETWEEN LIKE MATING TYPES IN THE YEAST SACCHAROMYCOPSIS-LIPOLYTICA BY PROTOPLAST FUSION.
AU STAHL U [Reprint author]
CS LEHRSTUHL ALLG BOT, RUHR-UNIV, POSTFACH 102148, D-4630 BOCHUM 1, W GER
SO Molecular and General Genetics, (1978) Vol. 160, No. 1, pp. 111-114.
CODEN: MGGEAE. ISSN: 0026-8925.
DT Article
FS BA
LA ENGLISH
AB Protoplasts from auxotrophic strains of the alkane yeast, S. (Candida) lipolytica, will hybridize despite identity in mating type. Fusion products following regeneration and selection form stable prototrophic diploids, and recombinant progeny can be obtained either through the parasexual or the sexual cycle. Mating type alleles of this yeast control only the initial steps in the mating sequence, cell recognition and agglutination, but not karyogamy and meiosis.

L5 ANSWER 19 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1977:124025 BIOSIS
DN PREV197763018889; BA63:18889
TI MORPHOGENESIS OF FILOBASIDIELLA-NEOFORMANS THE SEXUAL STATE OF CRYPTOCOCCUS-NEOFORMANS.
AU KWON-CHUNG K J
SO Mycologia, (1976) Vol. 68, No. 4, pp. 821-833.
CODEN: MYCOAE. ISSN: 0027-5514.
DT Article
FS BA
LA Unavailable
AB Morphogenesis of F. neoformans (= C. neoformans) was studied. A dikaryotic mycelium with clamp connections is formed after conjugation of 2 yeast cells of opposite mating type. A nonseptate, slender basidium with an abruptly expanded apex arises laterally or terminally from the dikaryotic hypha. The zygote nucleus in the basidium

undergoes meiosis and the 4 resulting haploid nuclei appear in the apical area of the basidium. As the nuclei divide by mitosis, uninucleate basidiospores are budded out from 4 spots on the apex of basidium. This basipetal budding produces long chains of basidiospores. Genetic analysis revealed a bipolar mating type system in this pathogen. The phylogenetic relationship of F. neoformans with other fungi is discussed.

L5 ANSWER 20 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1976:178182 BIOSIS
DN PREV197662008182; BA62:8182
TI REGULATION OF MATING AND MEIOSIS IN YEAST BY THE MATING TYPE REGION.
AU KASSIR Y; SIMCHEN G
SO Genetics, (1976) Vol. 82, No. 2, pp. 187-206. CODEN: GENTAE. ISSN: 0016-6731.
DT Article
FS BA
LA Unavailable
AB A supposed sporulation-deficient mutation of Saccharomyces cerevisiae is found to affect mating in haploids and in diploids and to be inseparable from the mating-type locus by recombination. The mutation is regarded as a defective a allele and is designated a*. This is confirmed by its dominance relations in diploids, triploids and tetraploids. Tetrad analysis of tetraploids and of their sporulating diploid progeny suggests the existence of an additional locus, RME, which regulates sporulation in yeast strains that can mate. Thus the recessive homozygous constitution rme/rme enables the diploids a*/α, a/a* and α/α to go through meiosis. Haploids carrying rme show apparent pre-meiotic DNA replication in sporulation conditions. This new regulatory locus is linked to the centromere of the mating-type chromosome, and its 2 alleles, rme and RME, are found among standard laboratory strains.

L5 ANSWER 21 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN
AN 1976:148630 BIOSIS
DN PREV197661048630; BA61:48630
TI THE MATING REACTION IN YEAST PART 2 SPONTANEOUS
OCCURRENCE OF OMNI MATING TYPES.
AU BLAMIRE J
SO Molecular and General Genetics, (1975) Vol. 141, No. 2, pp.
185-188.
CODEN: MGGEAE. ISSN: 0026-8925.
DT Article
FS BA
LA Unavailable

L5 ANSWER 22 OF 34 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN
AN 1974:18858 BIOSIS
DN PREV197410018858; BR10:18858
TI MUTATIONS WHICH ALTER MATING TYPE CONTROL OVER YEAST
SPORULATION.
AU HOPPER A K; HALL B D
SO Genetics, (1973) Vol. 74, No. 2 PT 2, pp. 119.
CODEN: GENTAE. ISSN: 0016-6731.
DT Article
FS BR
LA Unavailable

L5 ANSWER 23 OF 34 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:897664 CAPLUS
DN 138:132718
TI Localization of the (1,3)β-D-glucan synthase catalytic subunit
homologue Bgs1p/Cps1p from fission yeast suggests that it is
involved in
septation, polarized growth, mating, spore wall formation and
spore
germination
AU Cortes, Juan Carlos G.; Ishiguro, Junpei; Duran, Angel; Ribas,
Juan Carlos
CS Instituto de Microbiologia Bioquimica and Departamento de
Microbiologia y
Genetica, Consejo Superior de Investigaciones Cientificas
(CSIC)/Universidad de Salamanca, Salamanca, 37007, Spain
SO Journal of Cell Science (2002), 115(21), 4081-4096
CODEN: JNCSAI; ISSN: 0021-9533
PB Company of Biologists Ltd.
DT Journal
LA English
AB Schizosaccharomyces pombe Bgs1p/Cps1p has been identified as a
putative
(1,3)β-D-glucan synthase (GS) catalytic subunit with a possible

function during cytokinesis and polarized growth. To study this possibility, double mutants of cps1-12 and cdc septation mutants were made. The double mutants displayed several hypersensitive phenotypes and altered actin distribution. Epistasis anal. showed mutations prior to septum synthesis were dominant over cps1-12, while cps1-12 was dominant over the end of septation mutant cdc16-116, suggesting Bgs1p is involved in septum cell-wall (1,3)β-D-glucan synthesis at cytokinesis. We have studied the in vivo physiol. localization of Bgs1p in a bgs1Δ strain containing a functional GFP-bgs1+ gene (integrated single copy and expressed under its own promoter). During vegetative growth, Bgs1p always localizes to the growing zones: one or both ends during cell growth and contractile ring and septum during cytokinesis. Bgs1p localization in cdc septation mutants indicates that Bgs1p needs the medial ring and septation initiation network (SIN) proteins to localize properly with the rest of septation components. Bgs1p localization in the actin mutant cps8-188 shows it depends on actin localization. In addition, Bgs1p remains polarized in the mislocalized growing poles and septa of tea1-1 and tea2-1 mutants.

During the meiotic process of the life cycle, Bgs1p localizes to the mating projection, to the cell-to-cell contact zone during cell fusion and to the neck area during zygote formation. Also, Bgs1p localization suggests that it collaborates in forespore and spore wall synthesis.

During spore germination, Bgs1p localizes first around the spore during isotropic growth, then to the zone of polarized growth and finally, to the medial ring and septum. At the end of spore-cell division, the Bgs1p displacement to the old end occurs only in the new cell. All these data show that Bgs1p is localized to the areas of polarized cell wall growth and so we propose that it might be involved in synthesizing the lineal

(1,3)β-D-glucan of the primary septum, as well as a similar lineal
(1,3)β-D-glucan when other processes of cell wall growth or repair
are needed.
OSC.G 37 THERE ARE 37 CAPLUS RECORDS THAT CITE THIS RECORD (37 CITINGS)
RE.CNT 86 THERE ARE 86 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 24 OF 34 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2000:46291 CAPLUS
DN 132:219431
TI Mass mating method in combination with G418- and aureobasidin a-resistance
markers for efficient selection of hybrids from homothallic strains in
Saccharomyces cerevisiae
AU Nakazawa, Nobushige; Okawa, Kumiko; Sato, Toshitsugu; Enei, Hitoshi;
Harashima, Satoshi
CS Department of Biotechnology, Faculty of Bioresource Science, Akita
Prefectural University, Akita-shi, 010-0146, Japan
SO Journal of Bioscience and Bioengineering (1999), 88(5), 468-471
CODEN: JBBIF6; ISSN: 1389-1723
PB Society for Bioscience and Bioengineering, Japan
DT Journal
LA English
AB The authors have developed a mass mating method using the spore
suspensions of homothallic yeasts of Saccharomyces cerevisiae in
combination with dominant selective drug resistance markers, Tn601(903)
against geneticin and AUR1-C against aureobasidin A for the selection of
the hybrids. To examine the effectiveness of these markers in the mass
mating method, each marker was introduced into a homothallic wine yeast.
Using a mixed culture of spore suspensions from the resultant
transformants, many hybrids were screened by the drug resistance markers.
This method is more practical than the spore-to-spore mating method
because it does not require the use of a micromanipulator and many hybrids
are obtained at one time. The resultant hybrids could be utilized for
industrial brewing because plasmids, which are used to confer resistance
markers, are easily eliminated from the hybrids by cultivation in a medium

without drugs. The authors propose that the mass mating method using spore suspensions in combination with dominant selective geneticin- and aureobasidin A-resistance markers is useful for the selection of hybrids from industrial homothallic yeasts.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 25 OF 34 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1995:677964 CAPLUS
DN 123:161808
OREF 123:28623a,28626a
TI Elements of chromosome structure and function in fission yeast
AU Allshire, Robin C.
CS MRC Human Genetics Unit, Western General Hospital, Edinburgh, EH4 2XU, UK
SO Seminars in Cell Biology (1995), 6(2), 55-64
CODEN: SCEBE3; ISSN: 1043-4682
PB Academic
DT Journal; General Review
LA English
AB A review with 74 refs. on chromosome structure and function in fission yeast. The investigation of fission yeast chromosome structure and function has moved rapidly over the past 10 yr. The isolation of replication origins, telomeres and centromeres has allowed the development of minichromosomes, a yeast artificial chromosome (YAC)-like cloning system and investigations into chromosome segregation and behavior during mitosis and meiosis. Many mutants have been isolated which are defective in chromosome segregation. The development of the fluorescent in-situ hybridization (FISH) technique for use in S. pombe has allowed the localization of centromeres and telomeres throughout mitosis and meiosis. In combination with indirect immunofluorescence to detect spindle and chromosomal proteins, the FISH technique should further advance the understanding of fission yeast chromosome structure and function. The recent discovery of a heterochromatin-like structure mediating transcriptional repression at centromeres reinforces the notion that fission yeast centromeres are similar to those of larger eukaryotes.

Further characterization of such phenomena will accelerate the genetic
dissection of this important chromosomal element.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)

L5 ANSWER 26 OF 34 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1990:568786 CAPLUS
DN 113:168786
OREF 113:28571a,28574a
TI "Alternative self-diploidization" or "ASD" homothallism in Saccharomyces
cerevisiae: isolation of a mutant, nuclear-cytoplasmic interaction and
endomitotic diploidization
AU Ono, Bunichiro; Ishino-Arao, Yumiko; Takasugi, Kazuhiro; Taniguchi,
Miyuki; Fukuda, Misa; Fukui, Mitsuko; Miyakawa, Isamu; Sando, Nobundo
CS Fac. Pharm. Sci., Okayama Univ., Okayama, 700, Japan
SO Genetics (1990), 125(4), 729-38
CODEN: GENTAE; ISSN: 0016-6731
DT Journal
LA English
AB A mutant of S. cerevisiae representing a novel life cycle, named
"alternative self-diploidization" or "ASD" homothallism, was obtained
fortuitously. In this cycle, MATα (or MATa) haplophase and
MATα/MATα (or MATa/MATa) diplophase alternate. Germinated
cells are haploid and mating. They soon become nonmating and sporogenous
as they vegetatively grow. They sooner or later diploidize presumably via
endomitosis. The diploid cells haploidize via normal meiosis.
A single recessive nuclear mutation, named asd1-1, is responsible for
"ASD" homothallism. In the p0 cytoplasm, asd1-1 cells mate even if at a
low efficiency and fail to diploidize. Since pet mutations do not have
such effects, it was concluded that a certain mitochondrial function other
than respiration is required for manifestation of "ASD" homothallism.
I.e., "ASD" homothallism is the result of some sort of nuclear cytoplasmic
interaction.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L5 ANSWER 27 OF 34 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1989:36504 CAPLUS

DN 110:36504
OREF 110:6029a,6032a
TI Physical monitoring of meiotic and mitotic recombination in yeast
AU Haber, James E.; Borts, Rhona H.; Connolly, Bernadette; Lichten, Michael;
Rudin, Norah; White, Charles I.
CS Rosenstiel Basic Med. Sci. Res. Cent., Brandeis Univ., Waltham, MA, 02254,
USA
SO Progress in Nucleic Acid Research and Molecular Biology (1988), 35, 209-59
CODEN: PNMBAF; ISSN: 0079-6603
DT Journal; General Review
LA English
AB A review with 94 refs. on phys. anal. of meiotic and mitotic recombination
and gene conversion in Saccharomyces, including timing of meiotic recombination, characterization of meiotic mutants, detection of intermediates of meiotic recombination, and studies of recombination in
small intervals and between distant chromosomal locations. Also discussed
is phys. monitoring of mitotic gene conversion in yeast mitochondria and
of yeast mating-type switching.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L5 ANSWER 28 OF 34 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1988:584641 CAPLUS
DN 109:184641
OREF 109:30457a,30460a
TI Indirect control of sporulation by the mating type locus in yeast
AU Mitchell, Aaron P.
CS Dep. Biochem. Biophys., Univ. California, San Francisco, CA, 94143, USA
SO UCLA Symposia on Molecular and Cellular Biology, New Series (1987), 52(Transcr. Control Mech.), 147-57
CODEN: USMBD6; ISSN: 0735-9543
DT Journal
LA English
AB Saccharomyces cerevisiae Cells sporulate (undergo meiosis and form spores) in response to starvation only if they express both alleles
of the mating type locus: MATa and MATα. The simultaneous expression of MATa and MATα gives rise to a neg. regulator, a1-α2, that represses the set of haploid-specific genes. One haploid-specific gene, RME1, encodes an inhibitor of meiosis. Thus, a1-α2 promotes sporulation through repression of an inhibitor
of sporulation.

L5 ANSWER 29 OF 34 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1988:525651 CAPLUS
DN 109:125651
OREF 109:20855a,20858a
TI Genetic lines of the yeast Hansenula polymorpha. III. Mating type determination
AU Bodunova, E. N.; Boikova, S. G.; Donich, V. N.; Nesterova, G. F.
CS "Gidrolizprom" Sci.-Ind. Corp., Leningrad, USSR
SO Genetika (Moscow) (1988), 24(5), 808-18
CODEN: GNKAA5; ISSN: 0016-6758
DT Journal
LA Russian
AB The regular change of haploid and diploid phases is revealed in genetic stocks of H. polymorpha. Haploid meiotic segregants were subdivided into 4 groups for their ability to copulate, leading to zygote formation. No segregants within one group copulate with each other. Strains of the first and second groups are able to intercross and to mate with the strains of the third group. The latter group can mate not only with the strains of the first and second groups but also with the strains of the fourth group, these being able to only form hybrids with the strains of the third group. Expression and the mode of inheritance of sex types after hybridization via copulation or protoplast fusion indicate the digene biallele system of sex determination which occupies an intermediate position among the bipolar system of ascomycetes and the multiallelomorph tetrapolar system of basidiomycetes. It differes substantially from the latter by the unitarity of functions of both mating type loci.

L5 ANSWER 30 OF 34 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1986:145347 CAPLUS
DN 104:145347
OREF 104:22919a,22922a
TI ran1+ Controls the transition from mitotic division to meiosis in fission yeast
AU Beach, David; Rodgers, Linda; Gould, Jane
CS Cold Spring Harbor Lab., Cold Spring Harbor, NY, 11742, USA
SO Current Genetics (1985), 10(4), 297-311
CODEN: CUGED5; ISSN: 0172-8083
DT Journal

LA English
AB The genetic and physiol. control of meiosis in fission yeast was investigated. Nutritionally depleted h+/h+ diploid cells become irreversibly commited to meiosis immediately prior to the initiation of premeiotic S phase. Premeiotic DNA synthesis requires matP+, matM+, mei2+, and mei++ but not the mitotic cell cycle control gene, cdc2+. The ran1+ is an essential gene, loss of which provokes sexual conjugation, premeiotic DNA synthesis, pseudomeiosis and the sporulation of haploid cells. Evidently, sexual differentiation is achieved physiol. by the inhibition of ran1+ activity in a 2-step process. In the first step, partial inhibition of ran1+ in starved haploid cells, leads to cell cycle arrest in G1 followed by sexual conjugation. In the second step, a pathway requiring the matP+, matM+, and met3+ genes of the newly-formed zygote, further inhibits ran1+ and thereby commits the cell to meiosis. Gene mei2+ is required for meiotic commitment after full inhibition of ran1+. Gene ran1+ is normally essential for vegetative cell reproduction but is inessential in cells which have abnormally high levels of cAMP-dependent protein kinase. The ran1+ gene is proposed to encode a high controlled protein kinase which shares key substrates with cAMP-dependent protein kinase.
OSC.G 79 THERE ARE 79 CAPLUS RECORDS THAT CITE THIS RECORD (79 CITINGS)

L5 ANSWER 31 OF 34 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1975:560670 CAPLUS
DN 83:160670
OREF 83:25215a,25218a
TI Control of yeast sporulation by the mating-type locus
AU Hopper, Anita K.; Hall, Benjamin D.
CS Univ. Washington, Seattle, WA, USA
SO Spores (1975), 6, 138-46
CODEN: SPORAI; ISSN: 0584-9144
DT Journal
LA English
AB In Saccharomyces cerevisiae meiosis and spore formation as well as mating age are controlled by the mating-type locus. Diploid cells heterozygous for mating type (aα cells) are capable of sporulation,

but cannot mate; diploid cells homozygous for mating type (aα and
αα cells) can mate, but cannot sporulate. From homozygous
mating-type diploid strains mutants were obtained that are able to
sporulate. Some of these mutants are still able to mate as efficiently as
wild-type αα and aa cells. For each such strain, the mutant
gene which uncouples sporulation from mating type is unlinked to the
mating-type locus and functions equally well in aa and αα
diploid cells. Two assays were developed to identify haploid segregants
carrying such CSP mutations: (i) α haploids are mated to a wild-type
aaa triploid strain, and aa diploid segregants from the aaaα
tetraploids are scored for the ability to sporulate: (ii) mutant haploid
segregants are capable of premeiotic DNA synthesis. Using these assays,
it was shown that the CSP1 gene exerts a dominant effect upon sporulation.
Although only 20% of the CSP1 cells in a culture complete sporulation, all
of them carry out premeiotic DNA synthesis. Measurements of intragenic
recombination frequency for the entire CSP1 sporulating population
indicated that 25-29% as many recombinants were produced by CSP1 cells as
by aα cells. The results indicate that the CSP1 mutation uncouples
meiotic DNA synthesis, but not meiotic recombination from mating-type
regulation. It appears that mating type exerts control over sporulation
at more than 1 site.

L5 ANSWER 32 OF 34 EMBASE COPYRIGHT (c) 2009 Elsevier B.V. All rights
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AN 1996148681 EMBASE
TI Basic yeast methods.
AU Toyn, J.H. (correspondence)
CS Division of Yeast Genetics, Natl. Institute for Medical Research, Mill
Hill, London NW7 1AA, United Kingdom.
SO Methods in Molecular and Cellular Biology, (1994) Vol. 5, No. 5, pp.
249-254.
ISSN: 0898-7750 CODEN: MMCBEV
CY United States

DT Journal; Article
FS 004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
LA English
SL English
ED Entered STN: 4 Jun 1996
Last Updated on STN: 4 Jun 1996
AB The purpose of this article is to give practical help to the new yeast
worker from the day when the first yeast samples arrive in the laboratory
up until the first experiments. Basically, this involves the application
of standard microbiological procedures to yeast, including growth of yeast
cultures on plates and in liquid culture medium and storage of yeast.
However, there are many small details that are important for getting the
best results even from the simplest procedures, such as replica plating or
growing a log phase culture. Step-by-step methods for determination of a
yeast genotype, including the mating type, are
described. The first step in any experiment with yeast is to obtain
strains with appropriate genotypes. Thus, a procedure for meiotic
recombination of genes is described.

L5 ANSWER 33 OF 34 EMBASE COPYRIGHT (c) 2009 Elsevier B.V. All rights
reserved on STN
AN 1993111366 EMBASE
TI Rapid kinetics of mismatch repair of heteroduplex DNA that is formed
during recombination in yeast.
AU Haber, J.E. (correspondence); Ray, B.L.; Kolb, J.M.; White, C.I.
CS Department of Biology, Rosenstiel Center, Brandeis University, Waltham, MA
02254, United States.
SO Proceedings of the National Academy of Sciences of the United States of
America, (1993) Vol. 90, No. 8, pp. 3363-3367.
ISSN: 0027-8424 CODEN: PNASA6
CY United States
DT Journal; Article
FS 004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
LA English
SL English
ED Entered STN: 16 May 1993

Last Updated on STN: 16 May 1993
AB Homothallic switching of yeast mating type (MAT) genes is a highly efficient gene conversion process initiated by a double-strand break. The use of a galactose-inducible HO endonuclease gene has made it possible to analyze the synchronous progression of molecular intermediates during recombination. When MATa switches to MATα, a 3' single-stranded end of HO-cleaved MATDNA invades the homologous donor, HMLα, and initiates copying of new DNA sequences. These early steps of recombination can be detected by PCR amplification. When recombination is initiated in a strain carrying the MATa- stk T → A base pair substitution mutation located 8 bp to the right of the HO endonuclease cleavage site, the stk mutation is frequently included in heteroduplex DNA formed between MAT and HML and undergoes mismatch correction. We have followed the kinetics of mismatch repair of the stk mutation by determining the DNA sequence of the PCR-amplified early intermediates of recombination. Mismatch correction of heteroduplex DNA is quite rapid (t(1/2) = 6-10 min) compared to the 60 min required to complete repair of the double-strand break. Mismatch repair occurs soon after the 3'- ended MAT-stk strand invades HML and forms heteroduplex DNA. Moreover, nearly all the correction events are restorations, in which the invading MAT-stk strand is corrected to the genotype of the resident HML donor. This rapid restoration ensures that the net result will be a gene conversion at the MAT locus. Rapid and preferential mismatch repair of heteroduplex DNA has important implications in understanding meiotic recombination.

L5 ANSWER 34 OF 34 EMBASE
AN 1989003319 EMBASE
TI Life cycle of the budding yeast Saccharomyces cerevisiae.
AU Herskowitz, I.
CS Department of Biochemistry & Biophysics, University of California, San Francisco, CA 94143, United States.

SO Microbiological Reviews, (1988) Vol. 52, No. 4, pp. 536-553.
ISSN: 0146-0749 CODEN: MBRED3
CY United States
DT Journal; General Review; (Review)
FS 004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
LA English
SL English
ED Entered STN: 12 Dec 1991
Last Updated on STN: 12 Dec 1991
AB The life cycle of the budding yeast Saccharomyces cerevisiae has two broad aspects, cell proliferation and transitions between haploid and diploid cell types. Haploids mate to form diploids, and diploids undergo meiosis to form haploids. The life cycle of S. cerevisiae has an additional aspect beyond proliferation, mating, and meiosis: haploid yeast cells (of appropriate genotype) can exhibit a 'homothallic' life cycle, one in which a haploid cell can give rise to diploid cells capable of meiosis and spore formation. Yeast strains of other genotypes exhibit a 'heterothallic' life cycle, in which a haploid cell is unable to yield diploid cells.
Studies of S. cerevisiae have provided a molecular understanding of (i) the different types of yeast cells that participate in mating and meiosis (haploid types a and α and the diploid a/α cell) and (ii) the mechanism for homothallism. Cell specialization in S. cerevisiae is governed by a master regulatory locus, the mating-type locus (MAT), whose two alleles (MATa and MATα) code for regulatory proteins (one activator and two repressor activities). One of the repressor activities (a1-α2) requires products coded by both MAT alleles and thus acts as a molecular monitor for diploidy. These regulatory proteins govern transcription of different gene sets, including a-specific genes (expressed only in a cells), α-specific genes (expressed only in α cells), and haploid-specific genes (expressed in both a and α cells). The homothallic life cycle (ability of haploid cells to produce diploid cells) occurs because of mating-type interconversion: cells first change from one mating type to the other by a programmed genetic rearrangement. Then sibling cells mate to form an a/α diploid cell. Mating-type interconversion is thus a process in

which the master regulatory locus, MAT, is itself regulated. This review
presents an overview of the mating-type locus and how it regulates
transcription of other genes, as well as a description of the different
methods used for assaying mating and associated phenomena. The molecular
mechanism of mating-type interconversion ('cassette' transposition) is
summarized, and biological aspects of the switching process, genetic
variations that lead to a heterothallic life cycle, and different possible
mechanisms for homothallism are discussed. The review concludes with a
description of features of the life cycles of other organisms (the fission
yeast Schizosaccharomyces pombe, filamentous fungi such as Neurospora
crassa, and basidiomycetes such as Schizophyllum commune and Ustilago
maydis, as well as ciliates and algae).

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